

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: January 18, 2000, 21:02:06 ; Search time 3378.13 Seconds  
(without alignments)  
3935.252 Million cell updates/sec

Title: US-09-303-232-5  
Perfect score: 3109  
Sequence: 1 ggcacgagccgcccgaagt.....ggttaagtgtaccacattgcg 3109

Scoring table: IDENTITY\_NUC

Searched: 780561 seqs, 2137953050 residues

Database : GenEmbl.\*

Word size : 0

Number of hits that pass the threshold : 1561122

- 1: gb\_bal.\*
- 2: gb\_bal2.\*
- 3: gb\_bal.\*
- 4: gb\_bal.\*
- 5: gb\_bal.\*
- 6: gb\_bal.\*
- 7: gb\_bal.\*
- 8: gb\_bal.\*
- 9: gb\_bal.\*
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- 11: gb\_bal.\*
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- 13: gb\_bal.\*
- 14: gb\_bal.\*
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- 20: gb\_bal.\*
- 21: gb\_bal.\*
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- 25: gb\_bal.\*
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- 32: gb\_bal.\*
- 33: gb\_bal.\*
- 34: gb\_bal.\*
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- 36: gb\_bal.\*
- 37: gb\_bal.\*
- 38: gb\_bal.\*
- 39: gb\_bal.\*
- 40: gb\_bal.\*
- 41: gb\_bal.\*
- 42: gb\_bal.\*
- 43: gb\_bal.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	3029	97.4	3029	36	AF143847	AF143847 Heliothis
2	579.8	18.6	3629	36	AF143846	AF143846 Heliothis
3	379.6	12.2	1509	9	HSNACHRA7	Y08420 H.sapiens m
4	379.6	12.2	1509	9	HSNACHRA7	U40583 Human alpha
5	378	12.2	1551	3	BSA7	X93504 B.taurus mR
6	378	12.2	1551	3	BSA7	X70297 H.sapiens m
7	377.4	12.1	1559	10	HUMANA7A	L25827 Human a7 n1
8	376.4	12.1	1876	11	HSU62436	U62436 Human nicot
9	376.4	12.1	2106	12	RATNARAD	L31619 Rattus ratt
10	376.4	12.1	3030	12	S53987	S53987 nicotinic r
11	376	12.1	1876	5	AR055255	AR055255 Sequence
12	374.8	12.1	1848	12	MUSNARS	L37663 Mus musculus
13	367.4	11.8	1555	9	HSCHRNA7A	Z23141 H.sapiens C
14	349	11.2	2037	4	GGNARA7A	X68586 G.gallus mR
15	342.4	11.0	2896	4	GGANAREC	X52295 Chicken alp
16	326.8	10.5	2090	4	GGANAREC	X52296 Chicken alp
17	305.6	9.8	1512	9	HSNACHRA3A	Y08418 H.sapiens m
18	304.4	9.8	1884	9	HSNACHRA4	Y08421 H.sapiens m
19	304.4	9.8	3343	11	HSU62433	U62433 Human nicot
20	303.2	9.7	1910	10	HUMNAR	M37981 Human alpha
21	303	9.7	1833	9	HSNACHRA4G	X87629 H.sapiens m
22	302.8	9.7	2082	10	HUMNACHRA4A	L35901 Human nicot
23	302.8	9.7	2082	10	HUMNACHRA4A	AR037435 Sequence
24	302.2	9.7	2277	5	AR037435	AR037435 Sequence
25	302.2	9.7	1590	10	HSY16281	Y16281 Homo sapien
26	302.2	9.7	2684	11	HSU62431	U62431 Human nicot
27	301.8	9.7	1931	12	RATNAR	L10077 Rat neuroa
28	298.8	9.6	1584	41	HUMA3NARSP	M86383 Homo sapien
29	298.2	9.6	2095	12	RATNARAC	L31620 Rattus norv
30	297.6	9.6	1756	5	AR055253	AR055253 Sequence
31	296.6	9.5	2149	12	AF007212	AF007212 Rattus no
32	296.6	9.5	2327	12	RATNARAB	M15682 Rat nicotin
33	296.4	9.5	1956	3	BTACHRECA	X57032 B.taurus mR
34	291.6	9.4	1425	9	HSNACHRA3	X53529 H.sapiens H
35	288	9.3	2374	5	AR055254	AR055254 Sequence
36	286.8	9.2	2838	35	DMNARAS	Y15593 Drosophila
37	285.8	9.2	2068	5	AR055252	AR055252 Sequence
38	285	9.2	2067	35	HVNACHRA1	AT000399 Heliothis
39	284.4	9.1	1578	35	LMNACHRA2	AJ000391 Locusta m
40	284.2	9.1	1858	12	RATNARA	L31621 Rattus ratt
41	284.2	9.1	1932	12	RNACHRAR	X03440 Rat mRNA fo
42	282.2	9.1	1963	35	SGNAA1	X55439 S. gregaria
43	282.2	9.1	1700	12	AF145286	AF145286 Mus muscu
44	281.6	9.1	1828	35	CENCHRA1	X83887 C.elegans m
45	281.2	9.0	2197	12	RATNARB	L31622 Rattus ratt

ALIGNMENTS

RESULT 1

AF143847

LOCUS

DEFINITION

ACCESSION

NID

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

AF143847 3029 bp mRNA INV 27-MAY-1999  
Heliothis virescens putative nicotinic acetylcholine receptor alpha  
7-2 subunit mRNA, complete cds.  
AF143847  
GI:4895006  
tobacco budworm.  
Heliothis virescens  
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;  
Ditrysia; Noctuidae; Noctuidae; Noctuidae; Heliothinae; Heliothis.  
1 (bases 1 to 3029)  
Schulze, T., Oellers, N. and Adamczewski, M.  
Putative alpha subunits of insect nicotinic acetylcholine receptors  
more similar to vertebrate alpha 7 subunits and C. elegans Ce21  
than to other insect nicotinic acetylcholine receptor alpha



[illegible]

Qy	2761	taacttttgatctctogtcatcgataaagtctcaacttaactatcgatagcgtaaatata	2820
Db	2761	TAACTTTTGATCTCTCGTATCGATAAATGCTCACTTAACTATCGATAGGTAATTATA	2820
Qy	2821	actgttagtatacgtatcgggagtagtcactatgcacagaaatagtcattaattagga	2880
Db	2821	ACTGTTAGTATATCGATATGGGAGTAGTCATAGCATCGAANAATGATTAATTAGGA	2880
Qy	2881	atcggttgtggttaattgttatgcttagcggaaatattacaatgcgttgatcatcctaac	2940
Db	2881	ATCGGTTGTGTAAATGTTATGTTTAGCGAAATATTACAATGCTGTTGATATCACTAAC	2940
Qy	2941	catcacgtaaccatatgtataaattgaaatcacagaataatcgcgtggtattgtatata	3000
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Db	3001	AAATTTTtagaaaaaaaaaaaaaaaaaaaaa	3029

BVRNAEF2

### DEFINITION

**NID  
WESTON**

**KEYWORDS**  
**SOURCE**

1

AUTHORS	TITLE
...	...

10

## REFERENCE

**JOURNAL  
OF  
POST KEYNESIAN  
ECONOMICS**

## Source

3







Neopterygii: Teleostei; Euteleostei; Ostariophysi; Cypriniformes;  
Cyprinidae; Cyprininae; Rasbora; Danio.  
1 (bases 1 to 2873)  
Liao, E.C., Paw, B.H., Oates, A.C., Pratt, S.J., Postlethwait, J.H. and  
Zou, L.I.  
SCL/Tal-1 transcription factor acts downstream of cloche to specify  
hematopoietic and vascular progenitors in zebrafish  
98167906  
2 (bases 1 to 2873)  
Liao, E.C., Paw, B.H., Oates, A.C., Pratt, S.J., Postlethwait, J.H. and  
Zou, L.I.  
Direct Submission  
Submitted (30-JAN-1998) Hematology/Oncology, Harvard Medical  
School, 300 Longwood Avenue, Boston, MA 02115, USA  
Location/Qualifiers  
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/organism="Danio rerio"  
/db\_xref="taxon:7955"  
/chromosome="LG XXII"  
/map="centromeric"  
/cell\_type="hematopoietic progenitors; angioblasts"  
1. 2873  
/gene="tal-1"  
297. 1289  
/gene="tal-1"  
/note="basic helix-loop-helix transcription factor; SCL"  
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/product="stem cell leukemia protein"  
/protein\_id="AAC41264.1"  
/db\_xref="PIR:G2921801"  
/db\_xref="GI:2921801"  
/translation="MEKLSKEQPLPSAEGCASPPRGDGRGQEGTAAETGHRH  
PEELNGVAKTAHATHELAKAEVIELSRGGSDVIKRELKAEILSHKVVTELCRRP  
IPLPLPRDLSEIHVQLLPAYPPRSEHRCSTANWTFPATINSFAGDAEQYGM  
PSNRVKRRPAPYEIINDSOPKIVRIFNTSEFRQONVNGAFELKLLIHPHP  
KKLKNETLRAMKYINFLAKLLNDQDMVGGEAPARANRDSDATLVRRDLLQEMLS  
PNSGCGILLDGDASPESTEDQDSVGVQALCKRTTFFQTAGRCPCAYTDNRH"  
799 a 661 c 599 g 714 t  
BASE COUNT 799 a 661 c 599 g 714 t  
ORIGIN  
2.2%; Score 80; DB 4; Length 2873;  
Query Match 2.2%; Score 80; DB 4; Length 2873;  
Best Local Similarity 100.0%; Pred. No. 2.3e-32;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
3610 caaaaaaaaaaaaaactcgagagtacttcagagcgccggcccatgatatt 3669  
2780 CAAAAAAAAAAAAAAAAAATCGAGAGTACTTCTAGAGCGCGCGGCCCATCATTT 2839  
QY 3670 ccaccgggtgggtaccag 3689  
DB 2840 CCACCGGGGTGGGTACCAG 2859  
RESULT 3  
HSU48696 2370 bp mRNA PRI 13-JUL-1996  
LOCUS Human mariner-like element-containing mRNA, clone pCHMT1.  
DEFINITION U48696  
ACCESSION G1399459  
NID G1399459  
VERSION GI:1399459  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 2370)  
AUTHORS Kiyosawa, H. and Chance, P.F.  
TITLE Primate origin of the CMT1A-REP repeat and analysis of a putative  
transposon-associated recombinational hotspot  
JOURNAL Hum. Mol. Genet. 5 (6), 745-753 (1996)  
MEDLINE 96372809

Thu Jan 20 07:41:56 2000

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OM nucleic - nucleic search, using sw model  
Run on: January 18, 2000, 21:00:23 ; Search time 3378.13 Seconds  
(without alignments)  
4683.317 Million cell updates/sec

Title: US-09-303-232-3  
Perfect score: 3700  
Sequence: 1 ggcacgagccgtgccccac.....gggtaccagtaagtgtaccc 3700

Scoring table: IDENTITY\_NUC  
Searched: 780561 seqs, 2137953050 residues

Database: GenEmbl.\*

Word size: 0  
Number of hits that pass the threshold: 1561122

- 1: gb\_ba1.\*
- 2: gb\_ba2.\*
- 3: gb\_cm.\*
- 4: gb\_ov.\*
- 5: gb\_pat.\*
- 6: gb\_ph.\*
- 7: gb\_pl1.\*
- 8: gb\_pl2.\*
- 9: gb\_pr1.\*
- 10: gb\_pr2.\*
- 11: gb\_pr3.\*
- 12: gb\_ro.\*
- 13: gb\_sts.\*
- 14: gb\_sy.\*
- 15: gb\_un.\*
- 16: gb\_v1.\*
- 17: em\_fun.\*
- 18: em\_htg.\*
- 19: em\_hum1.\*
- 20: em\_hum2.\*
- 21: em\_in.\*
- 22: em\_on.\*
- 23: em\_ov.\*
- 24: em\_ov.\*
- 25: em\_pat.\*
- 26: em\_ph.\*
- 27: em\_pl.\*
- 28: em\_ro.\*
- 29: em\_sts.\*
- 30: em\_sy.\*
- 31: em\_un.\*
- 32: gb\_htg1.\*
- 33: gb\_v1.\*
- 34: gb\_htg2.\*
- 35: gb\_in1.\*
- 36: gb\_in2.\*
- 37: em\_ba1.\*
- 38: em\_ba2.\*
- 39: em\_hum3.\*
- 40: em\_hum4.\*
- 41: gb\_pr4.\*
- 42: gb\_htg3.\*
- 43: gb\_htg4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	3617	97.8	3629	36	AF143846	AF143846 Heliothis
2	379.8	15.7	3029	36	AF143847	AF143847 Heliothis
3	410.6	11.1	1848	12	MUSNARS	L37663 Mus musculus
4	405.6	11.0	1876	11	HSU62436	U62436 Human nicot
5	405.2	11.0	1876	5	AR055255	AR055255 Sequence
6	404.6	10.9	3030	12	S53987	S53987 nicotinic r
7	404	10.9	1509	9	HSNACHRA7	Y08420 H.sapiens m
8	403	10.9	2087	9	HSARA7A	X70297 H.sapiens m
9	401.8	10.9	2106	12	RATNARAD	L31619 Rattus ratt
10	400.8	10.8	1977	10	HSU40583	U40583 Human alpha
11	397.6	10.7	1555	9	HSCHRNA7A	223141 H.sapiens C
12	396.4	10.7	1551	3	BTA7	X93604 B.taurus mr
13	396	10.7	1559	10	HUMA7NAR	L25827 Human a7 ni
14	345.6	9.3	2067	35	HVNACHRA1	AF000399 Heliothis
15	333.4	9.0	2037	4	GGNARA7A	X65886 G.gallus mr
16	327.4	8.8	2696	4	GGN7NAREC	X52295 Chicken alp
17	325.6	8.8	1963	35	SGNARAL1	X54339 S. gregaria
18	324.4	8.8	1578	35	LMNACHRA2	AJ000391 Locusta m
19	312.2	8.4	2090	4	GA8NAREC	X52296 Chicken alp
20	311.8	8.4	1623	35	LMNACHRA3	AJ000392 Locusta m
21	309.2	8.4	2277	5	AR037435	AR037435 Sequence
22	309.2	8.4	1590	10	HSY16281	Y16281 Homo sapien
23	309.2	8.4	2664	11	HSU62432	U62432 Human nicot
24	299	8.1	1908	11	HSU62432	U62432 Human nicot
25	295.8	8.0	1824	35	MSNARALPH	L35901 Human nicot
26	295.8	8.0	1756	5	AR055253	X08795 M.sexta mrn
27	295.4	8.0	1343	11	HSU62433	AR055253 Sequence
28	295.2	8.0	1956	3	BTACHRECA	U62433 Human nicot
29	294.6	8.0	2450	5	AR055256	X57032 B.taurus mr
30	293.6	7.9	1771	9	HSACHRB2	AR055256 Sequence
31	293.6	7.9	2448	11	HSU62437	X53179 Human mrna
32	293.6	7.9	2068	5	AR055252	U62437 Human nicot
33	292.8	7.8	1512	9	HSNACHRA3	AR055252 Sequence
34	288.2	7.8	1833	9	HSNACHRA4	Y08418 H.sapiens m
35	288	7.8	1836	11	AF037646	AF037646 Homo sapi
36	286.2	7.7	1833	9	HSNACHRA4	X87629 H.sapiens m
37	285.6	7.7	3618	3	BTACHRA1	X02509 B.taurus mr
38	285.2	7.7	1910	10	HUMNAR	X37981 Human alpha
39	285	7.7	1509	9	HSNACHRB2	Y08415 H.sapiens m
40	284.6	7.7	1884	9	HSNACHRA4	Y08421 H.sapiens m
41	284.4	7.7	1860	12	MUSACHRA2	M17640 Mus musculu
42	281.8	7.6	1521	5	AR037436	AR037436 Sequence
43	280.8	7.6	2838	35	DMNARAS	Y15593 Drosophila
44	280.6	7.6	1584	41	HUMA3NARSP	M86383 Homo sapien
45	280.4	7.6	2374	5	AR055254	AR055254 Sequence

ALIGNMENTS

RESULT 1

AF143846

LOCUS

DEFINITION

ACCESSION

NID

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

AF143846 3629 bp mRNA INV 27-MAY-1999  
Heliothis virescens putative nicotinic acetylcholine receptor alpha  
7-1 subunit mRNA, complete cds.

AF143846  
94895004  
AF143846.1 GI:4895004

tobacco budworm.  
Heliothis virescens  
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;  
Ditrysia; Noctuoidea; Noctuidae; Heliothinae; Heliothis.

1 (bases 1 to 3629)  
Schulze, T., Oellers, N. and Adamczewski, M.  
Putative alpha subunits of insect nicotinic acetylcholine receptors  
more similar to vertebrate alpha 7 subunits and C. elegans Ce21  
than to other insect nicotinic acetylcholine receptor alpha







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OM nucleic - nucleic search, using sw model

Title: US-09-303-232-1  
 Perfect score: 2886  
 Sequence: 1 qcacacgagagaaagattgtgg.....aaaaaaaaaaaaaaaaaaaaa 2886

Scoring table: OLIGO\_NUC  
Searched: 780561 seqs, 2137953050 residues  
Database: GenEmbl.\*

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Word size : 14
Number of bits that pass the threshold : 99869
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Number of hits that pass the threshold : 99869

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1: gb_bal:*
2: gb_ba2:*
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4: gb_ov:*
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8: gb_pl2:*
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10: gb_pr2:*
11: gb_pr3:*
12: gb_ro:*
13: gb_sts:*
14: gb_sy:*
15: gb_un:*
16: gb_vi:*
17: em_fun:*
18: em_htg:*
19: em_hum1:*
20: em_hum2:*
21: em_in:*
22: em_om:*
23: em_or:*
24: em_ov:*
25: em_pat:*
26: em_ph:*
27: em_pl1:*
28: em_ro:*
29: em_sts:*
30: em_sy:*
31: em_un:*
32: em_vi:*
33: gb_htg1:*
34: gb_htg2:*
35: gb_in1:*
36: gb_in2:*
37: em_bal:*
38: em_ba2:*
39: em_hum3:*
40: em_hum4:*
41: gb_pr4:*
42: gb_htg3:*
43: gb_htg4:*

```

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	573	19.9	76947	35	AC004326	AC004326 Drosophill
C 2	35	1.2	3629	36	AF143846	AF143846 Heliothis
C 3	31	1.1	355	13	AUF66809	U66809 Astatoeoch
C 4	31	1.1	41602	42	AC010017	AC010017 Drosophill
C 5	31	1.1	127189	43	AC010995	AC010995 Drosophill
C 6	30	1.0	721	9	HSSRP14A	X73459 H.sapiens m
C 7	30	1.0	442	11	HSU92988	U92988 Homo sapien
C 8	30	1.0	201986	12	AC006289	AC006289 Mus muscu
C 9	30	1.0	201964	12	MMXCK25N7	AF030001 Mus muscu
C 10	30	1.0	4552	36	AF064258	AF064258 Strongylo
C 11	29	1.0	2782	35	S79891	S79891 sr-stripe (
C 12	29	1.0	3568	35	SUSOCT6IND	LO4846 Strongyloce
C 13	29	1.0	4714	36	AF181637	AF181637 Drosophill
C 14	29	1.0	159507	41	AC004985	AC004985 Homo sapi
C 15	29	1.0	135098	43	AC007518	AC007518 Mus muscu
C 16	28	1.0	130663	34	AC007808	AC007808 Drosophill
C 17	28	1.0	122869	34	AC008895	AC008895 Homo sapi
C 18	28	1.0	155135	43	AC011087	AC011087 Homo sapi
C 19	27	0.9	846	8	ATHMGALPH	X14071 Arabidopsis
C 20	27	0.9	162822	11	AC005751	AC005751 Homo sapi
C 21	27	0.9	159040	34	AC007185	AC007185 Drosophill
C 22	27	0.9	87585	35	AC004239	AC004239 Drosophill
C 23	27	0.9	4771	35	DMAEDBC1A	X51663 D.melanogas
C 24	27	0.9	3885	35	DMAEDBP3	X16134 Drosophila
C 25	27	0.9	338234	35	DMU31961	U31961 Drosophila
C 26	27	0.9	80423	35	DROABD8	L07835 Drosophila
C 27	27	0.9	4976	36	DMU19269	U19269 Drosophila
C 28	26	0.9	2508	4	AF032896	AF032896 Petromyzo
C 29	26	0.9	1515	4	CHKVITB	K02113 Gallus gall
C 30	26	0.9	5791	4	CHKVITC	M18060 Chicken vit
C 31	26	0.9	20343	4	GGVITIG	X13607 Chicken vit
C 32	26	0.9	11132	7	FERRNA	X80212 F.hygrometr
C 33	26	0.9	4673	7	YSCUGA35	M63498 S.cerevisia
C 34	26	0.9	125502	8	ATY4L20	AL023094 Arabidops
C 35	26	0.9	660	8	CNS019Y5	AL112245 Botrytis
C 36	26	0.9	696	8	CNS01BD5	AL114081 Botrytis
C 37	26	0.9	114498	8	F309	AC006341 Arabidops
C 38	26	0.9	408	9	ASBO18516	AB018516 Homo sapi
C 39	26	0.9	162383	9	AB023054	AB023054 Homo sapi
C 40	26	0.9	162383	9	AB023055	AB023055 Homo sapi
C 41	26	0.9	100000	9	AP000517	AP000517 Homo sapi
C 42	26	0.9	103817	9	HS1216H12	AL008715 Homo sapi
C 43	26	0.9	114231	9	HS390C10	AL008721 Homo sapi
C 44	26	0.9	114771	9	HS569D19	AL022334 Homo sapi
C 45	26	0.9	185001	34	AC007366	AC007366 Human DNA

## ALIGNMENTS

[illegible]

